

ADIPROT = *Mycoplasma arginini*
ARTADIPRO = *Mycoplasma arthritides*
HOMADIPRO = *Mycoplasma hominus*

2/10

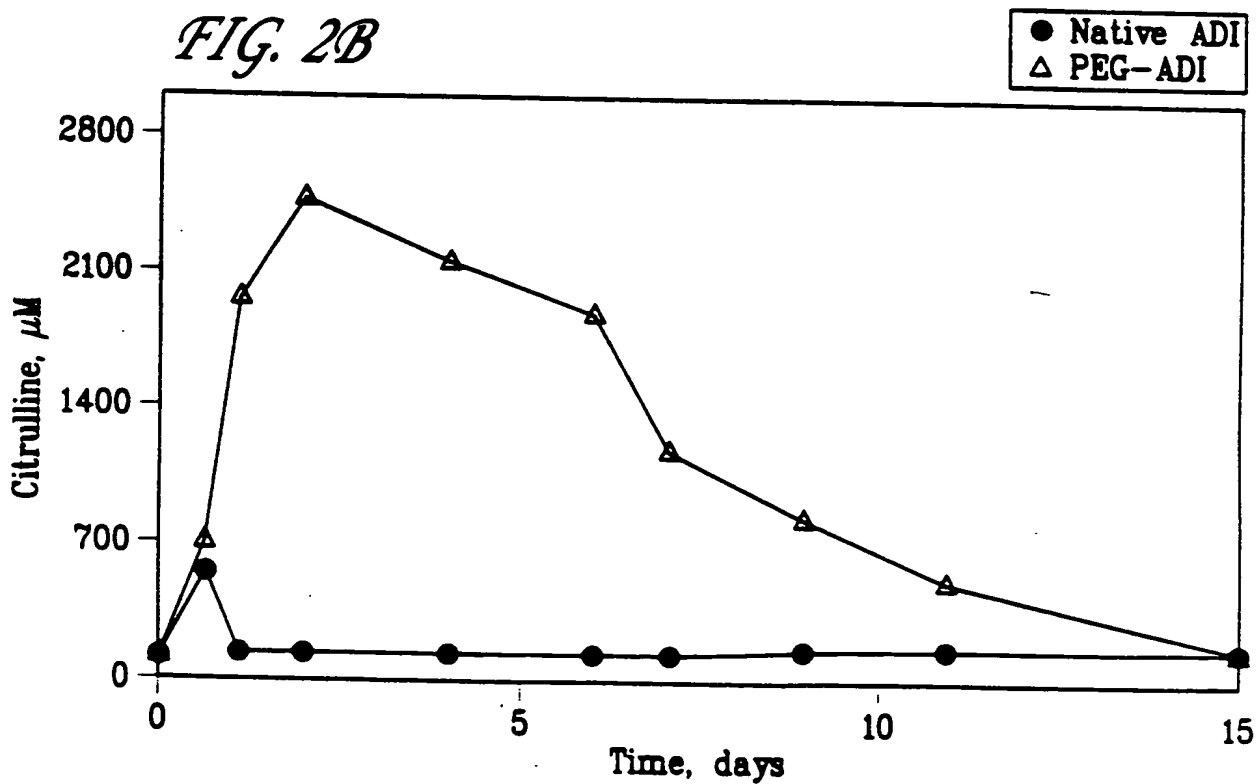
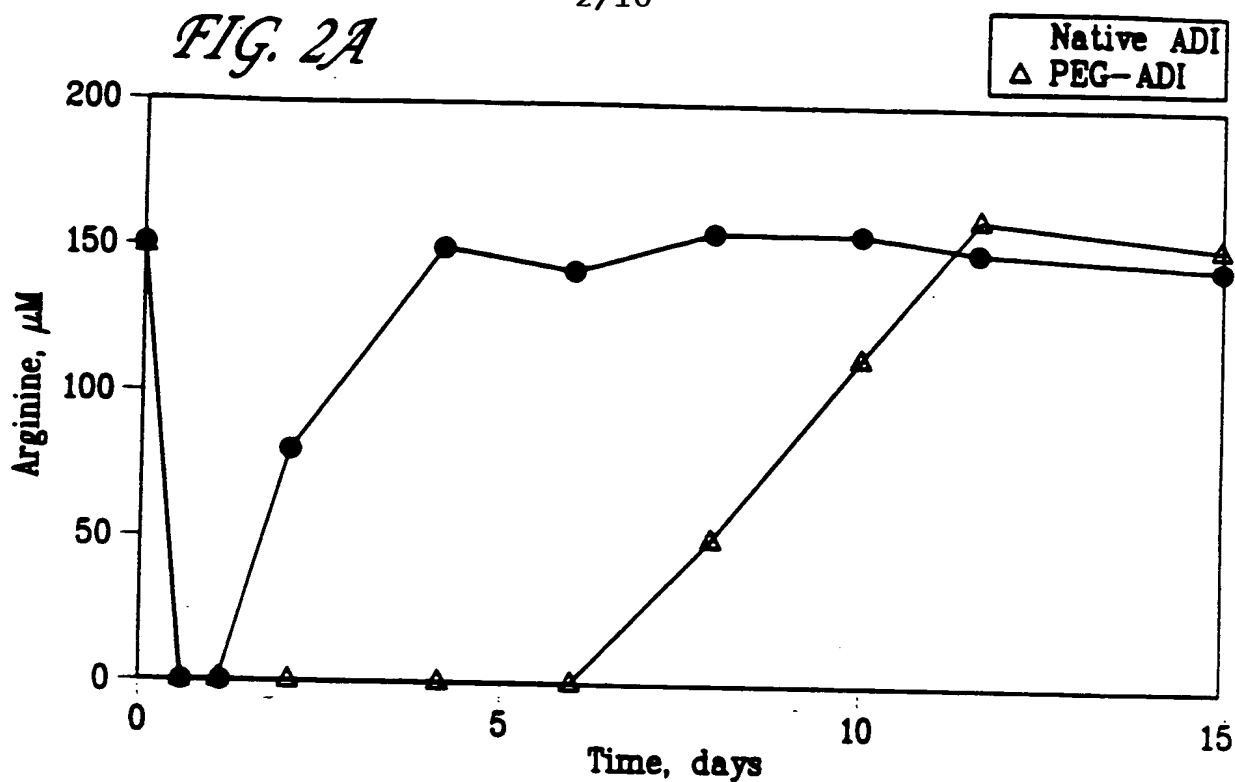


FIG. 3 3/10

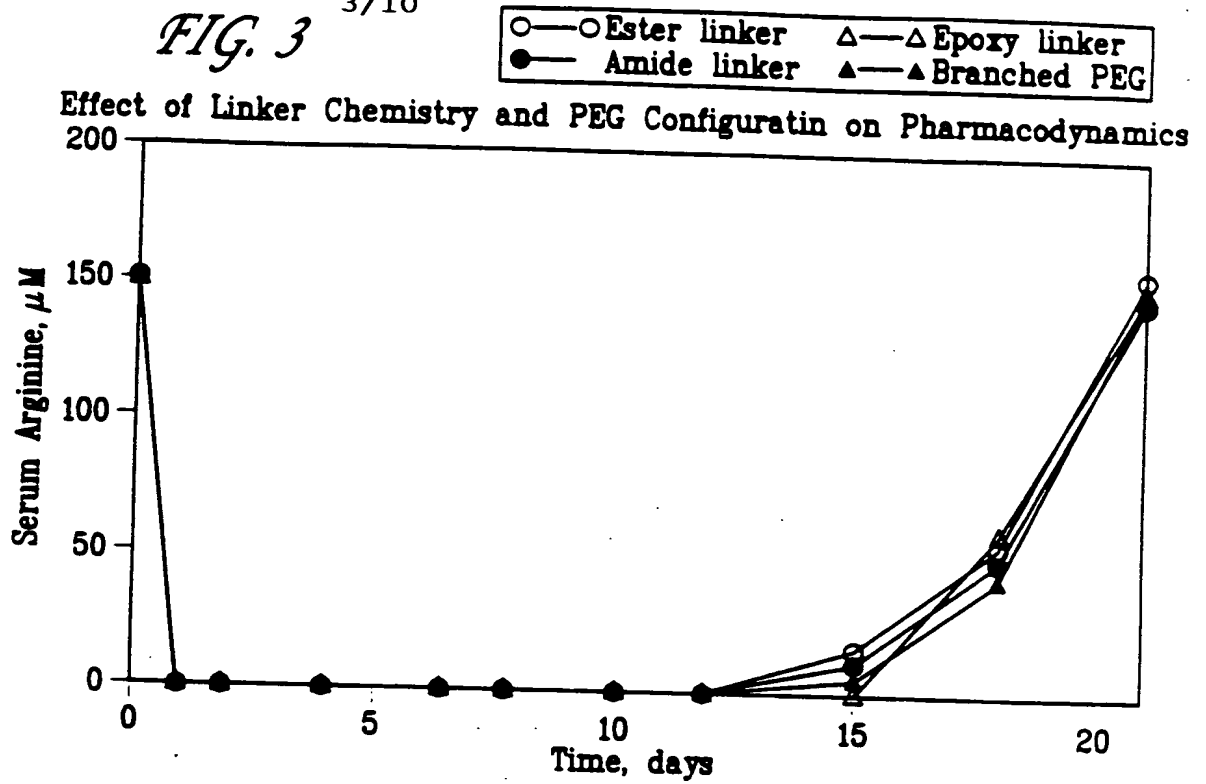
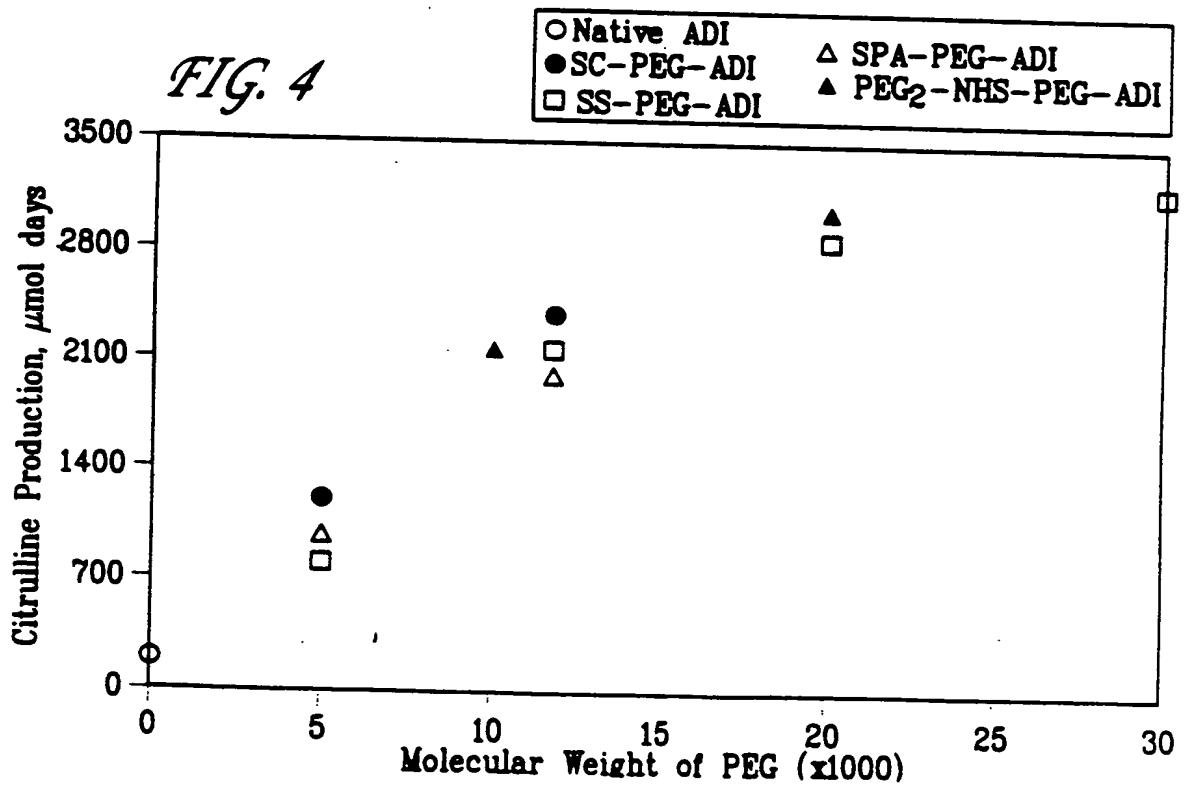
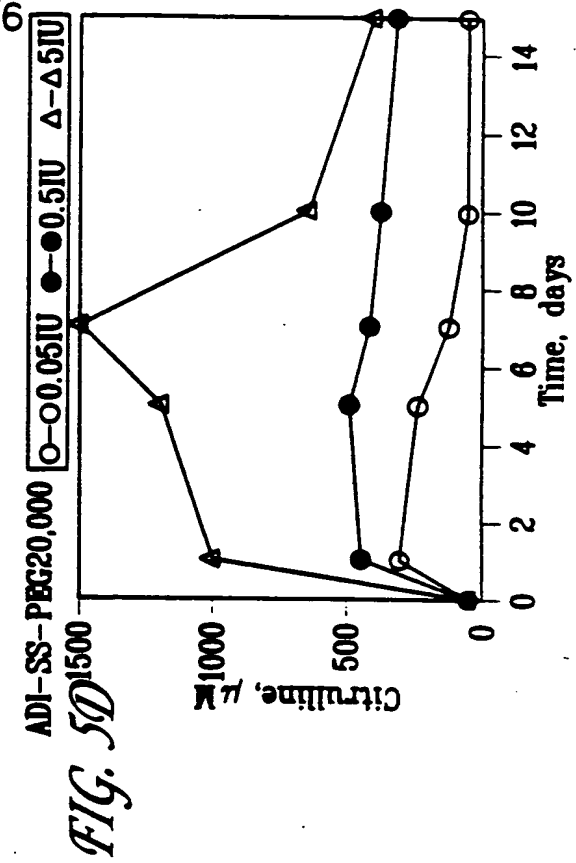
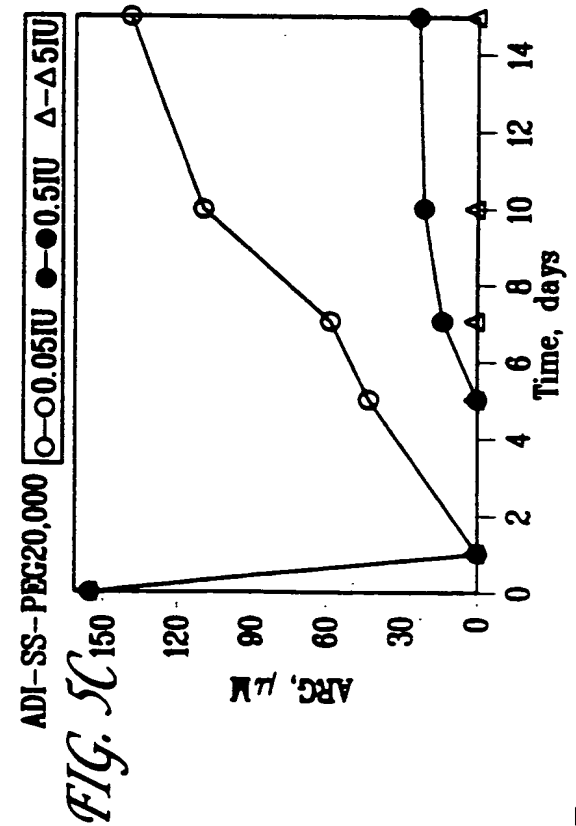
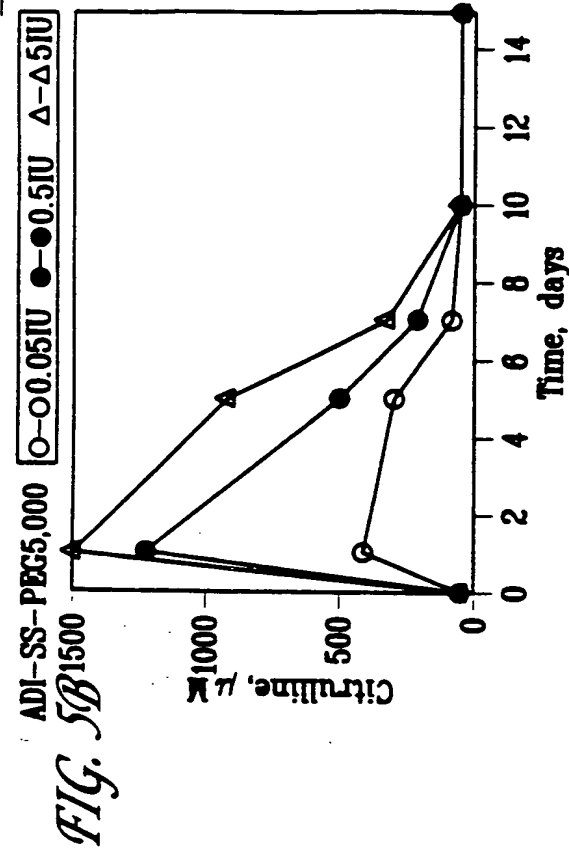
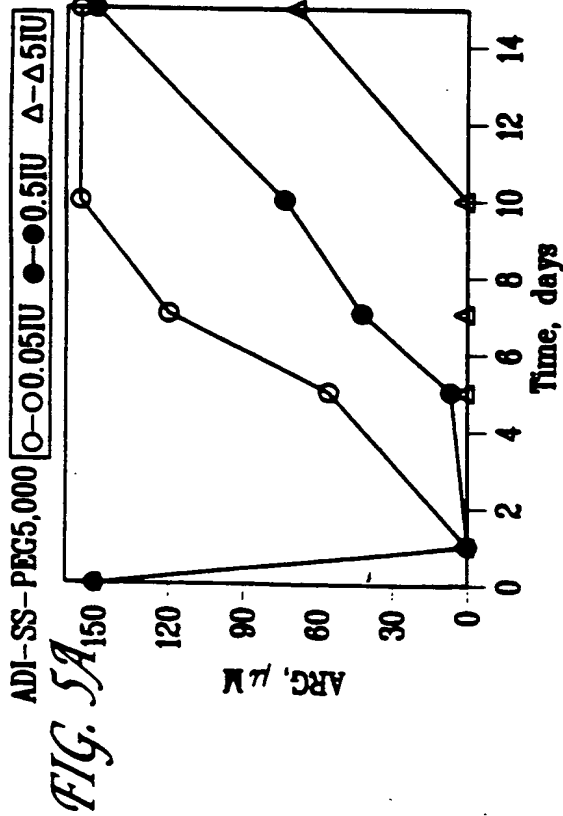


FIG. 4





4/10
4/6

5/10

FIG. 6

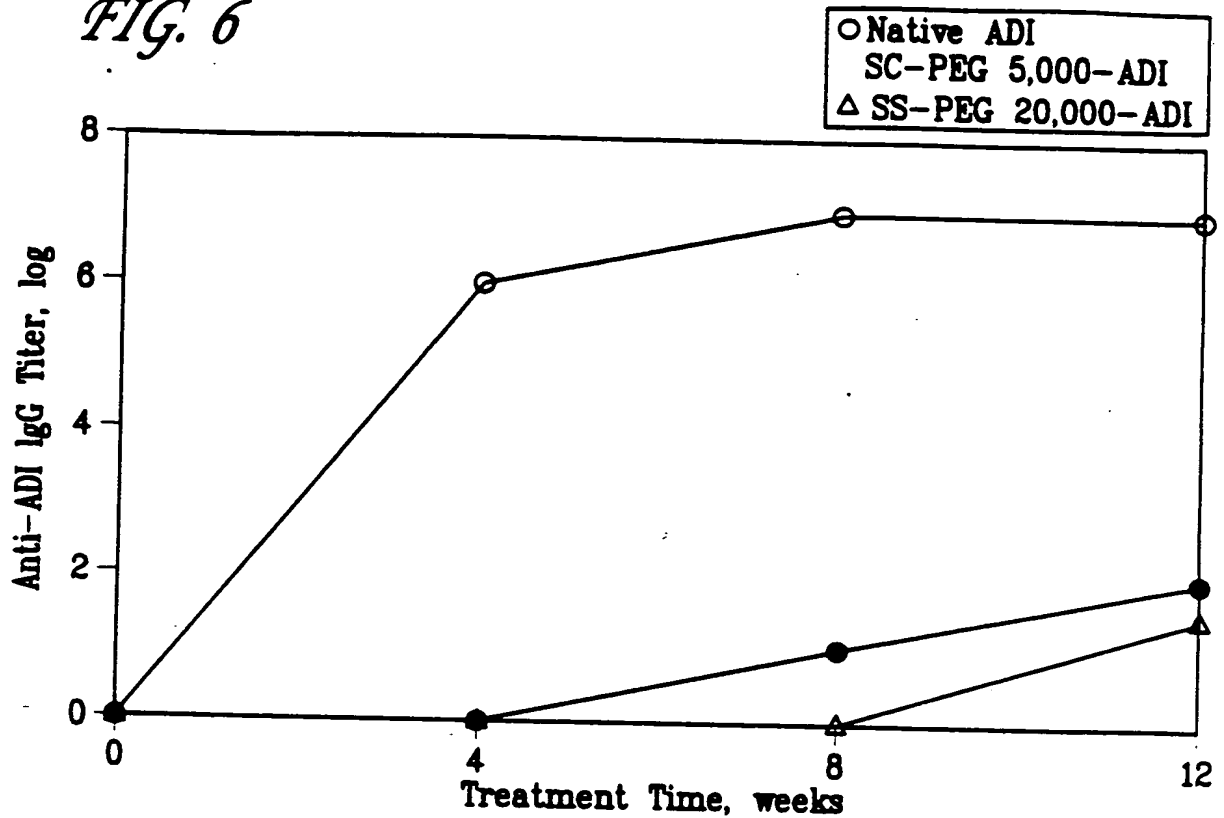
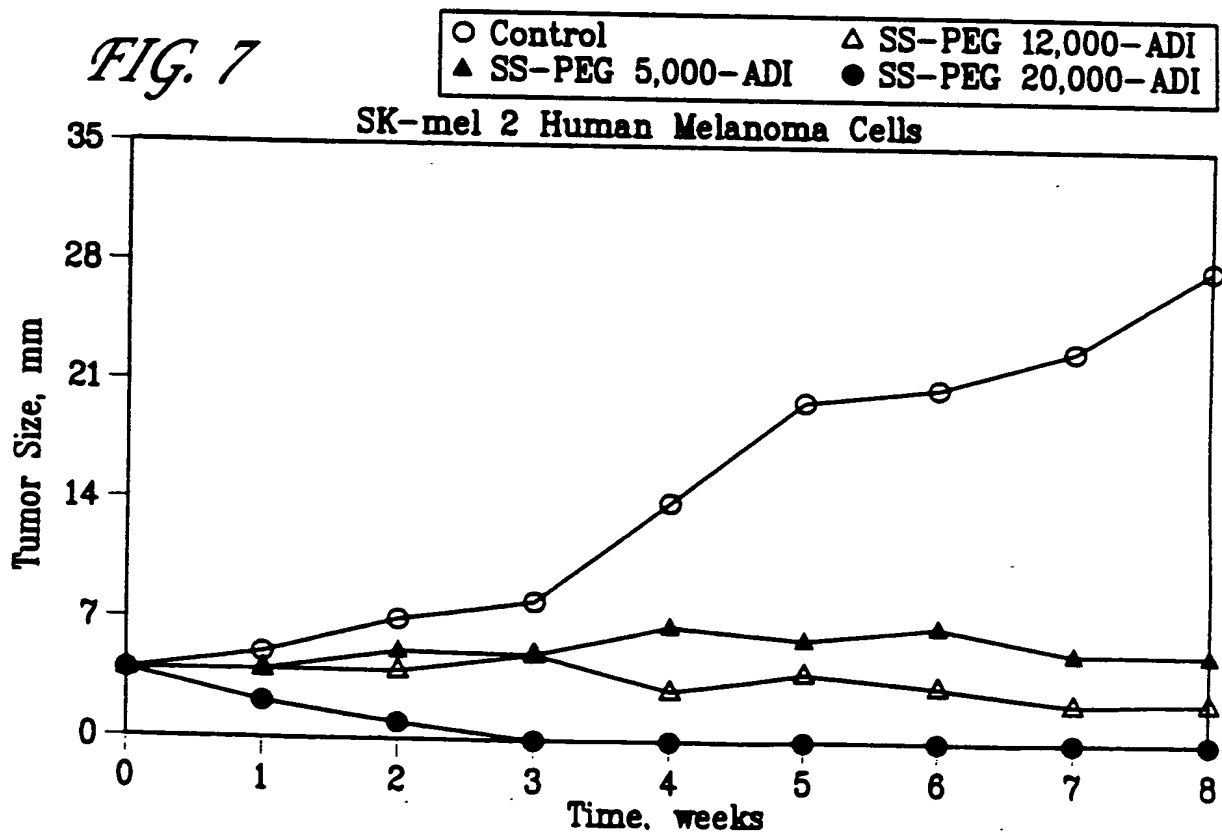


FIG. 7



6/10

FIG. 8

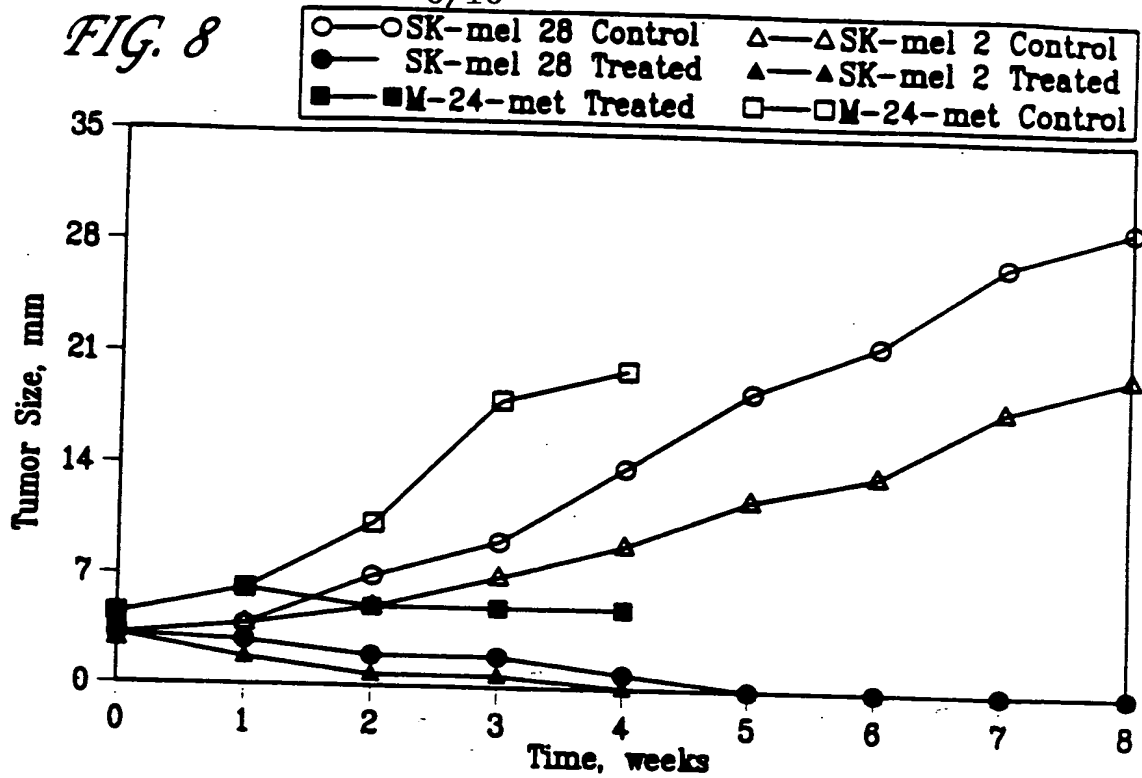
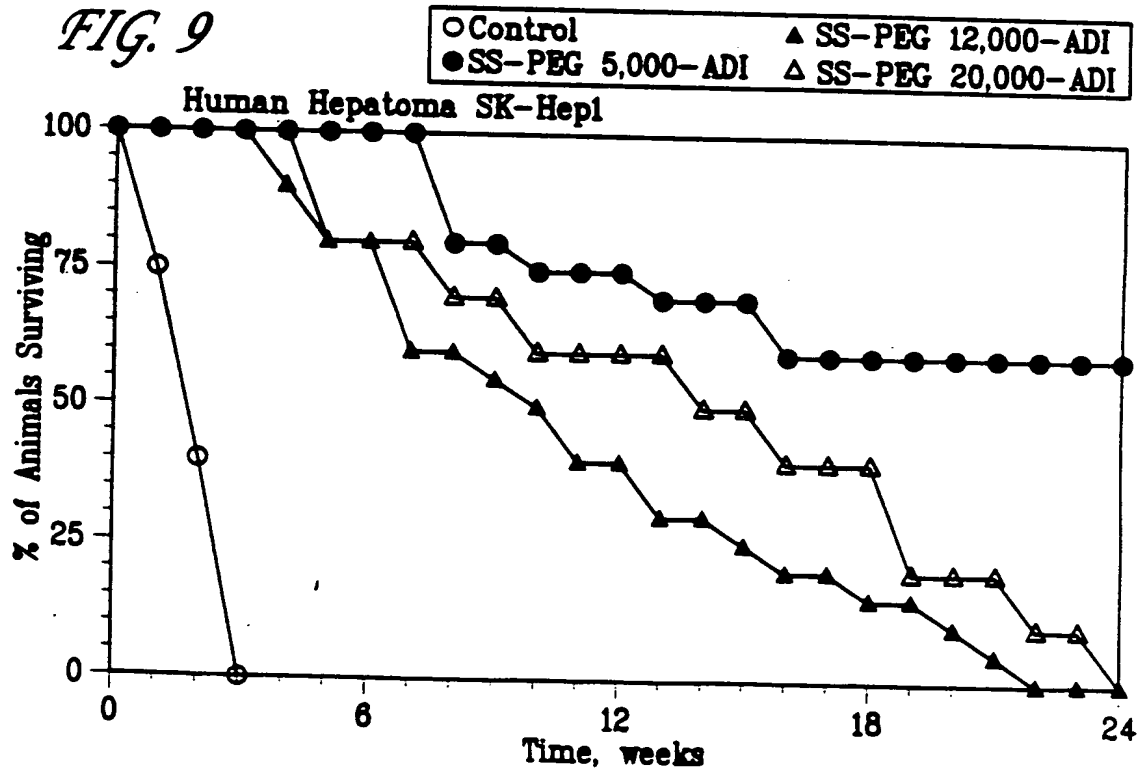


FIG. 9



The alignment was done on 2 amino acid sequences. 7/10

Alignment

STRADIPYR	MTAQTPIHVYSEIGKLKKVLLHRPGKEIENLMPDYLERLLFDDIPFLEDA	50
STRADIPNE	MSSHPIQVFSEIGKLKKVMLHRPGKELENLLPDYLERLLFDDIPFLEDAQ	50
STRADIPYR	QKEHDAFAQALRDEGIEVLYLETLAAESLVTPEIREAFIDEYLSEANIRG	100
STRADIPNE	KEHDAFAQALRDEGIEVLYLEQLAAESLTSPEIRDQFIEEYLDEANIRDR	100
STRADIPYR	RATKKAIRELLMAIEDNQELIEKTMAGVQKSELPEIPASEKGLTDLVESN	150
STRADIPNE	QTKVAIRELLHGIKDNQELVEKTMAGIQKVELPEIPDEAKDLTDLVESEY	150
STRADIPYR	YPFAIDPMPNLYFTRDPFATIGTGVSLSNHMFSETRNRETLYGKYIFTHHP	200
STRADIPNE	PFAIDPMPNLYFTRDPFATIGNAVSLNHMFADTRNRETLYGKYIFKYHPI	200
STRADIPYR	IYGGGKVPVMVYDRNETTRIEGGDELVLSKDVLA VGISQRTDAASIEKLLV	250
STRADIPNE	YGGKVDLVYNREEDTRIEGGDELVLSKDVLA VGISQRTDAASIEKLLVNI	250
STRADIPYR	NIFKQNLGFKKVLAFEFANNRKFMHLDTVFTMVDYDKFTIHPEIEGDLRV	300
STRADIPNE	FKKNVGFKKVLAFEFANNRKFMHLDTVFTMVDYDKFTIHPEIEGDLHVYS	300
STRADIPYR	YSVTYDNEELHIVEEKGD LAELLAANLGVEKVDLIRCGGDNLVAAGREQW	350
STRADIPNE	VTYENEKLKIVEEKGD LAELLAQNLGVEKVHLIRCGGNIVAAAREQWND	350
STRADIPYR	NDGSNTLTIAPGVVVVYNRNTITNAILESKGLKLIKIHGSELVRGRGGPR	400
STRADIPNE	GSNTLTIAPGVVVVYDRNTVTNKILEEYGLRLIKIRGSELVRGRGGPRCM	400
STRADIPYR	CMSMPFEREDI	411
STRADIPNE	SMPFEREEV	409

FIG. 10

STRADIPYR = *Streptococcus pyogenes*

STRADIPNE = *Streptococcus pneumoniae*

The alignment was done on 2 amino acid sequences. 8/10

Alignment

BORADIBUR	MEEEYLNPNIFSEIGRLKKVLLHRPGELENLTPLIMKNFLFDDIPYLK	50
BORADIAFZ	MEEYLNPNIFSEIGRLKKVLLHRPGELENLTPFIMKNFLFDDIPYLEV	50
BORADIBUR	VARQEHEVFVNILKDNSVEIEYVEDLVSEVLASSVALKNKFISQFILEAE	100
BORADIAFZ	ARQEHEVFASILKNNLVEIEYIEDLISEVLVSSVALENKFISQFILEAEI	100
BORADIBUR	IKTDGVINILKDYFSNLTVDNMVSKMISGVAREELKDCEFSLDDWVNGSS	150
BORADIAFZ	KTDFTINLLKDYFSSLTIDNMISKMISGVVTEELKNYTSSLDDLNGANL	150
BORADIBUR	FVIDPMPNVLFTRDPFASIGNGITINKMYTKVRRRETIFAHEYIFKYHSAY	200
BORADIAFZ	FIIDPMPNVLFTRDPFASIGNGVTTINKMFTKVRQRETIFAHEYIFKYHPVY	200
BORADIBUR	KENVPIWFNRWEETSLEGGDEFVLNKDLLVIGISERTEAGSVEKLAASLF	250
BORADIAFZ	KENVPIWLNRWEEASLEGGDELVLNKGLLVIGISERTEAKSVEKLAISLF	250
BORADIBUR	KNKAPFSTILAFKIPKNRAYMHLDTVFTQIDYSVFTSFTSDDMYFSIYVL	300
BORADIAFZ	KNKTSFDTILAFQIPKNRSYMHLDTVFTQIDYSVFTSFTSDDMYFSIYVL	300
BORADIBUR	TYNSNSNKNIKKEKAKLKDVLFSYLGRKIDIICAGGDLIHGAREQWND	350
BORADIAFZ	TYNPSSSKIHIKKEKARIKDVLSFYLGKIDIICAGGDLIHGAREQWND	350
BORADIBUR	GANVLAIAAPGEVIAYSRNHVTKLFEENGIVHRIPSSSELSRGRGGPRCM	400
BORADIAFZ	GANVLAIAAPGEIAYSRNHVTNKLFEENGIVHRIPSSSELSRGRGGPRCM	400
BORADIBUR	SMSLVREDI	409
BORADIAFZ	SMPLIREDI	409

FIG. 11

BORADIBUR = *Borrelia burgdorferi*
 BORADIAFZ = *Borrelia afzellii*

The alignment was done on 3 amino acid sequences.

9/10

Alignment

QIAADIINT	MTDFSKDKEKLAQATQGGENERAEIVVVHLPQGTSTSLNPEGNNLEEP	50
CLOADIPER	MRDDRALNVTSEIGRLKTVLLHRPGEEIENLTPDLLDRLLFDDIPYLKVA	50
BACADILIC	MIMTTPIHVYSEIGPLKTVMLKRPGRELENLTPEYLERLLFDDIPFLPAV	50
QIAADIINT	ICPDELRRDHGEGFAVLKEKGCRVYMPYDVLSEASPAEREVLMDQAMASL	100
CLOADIPER	REEHDAFAQTLREAGVEVLYLEVLAAEAIETSDEVKQQFISEFIDEAGVE	100
BACADILIC	QKEHDQFAETLKQQGAEVLYLEKLTAEALDDALVREQFIDELLTESKADI	100
QIAADIINT	KYELHATGARITPKMKYCVSDEYKRKVLSTALSTRNLVDVILSEPVHILAP	150
CLOADIPER	SERLKEALIEYFNSFSDNKAMVDKMMAGVRKEELKDYHRESLYDQVNNVY	150
BACADILIC	NGAYDRLKEFLLTFDADSMVEQVMGIRKNELEREKSKSHLHELMEDHYPF	150
QIAADIINT	GVRNTALVTNSVEIHDSNNMVFMRDQQITTRRGIVMGQFQAPORRREQVL	200
CLOADIPER	PFVCDPMPNL YFTREPFA TIGHGITLNMRTDTRNRETIFAKYIFRHHPR	200
BACADILIC	YLDPMPNLYFTRDPA AIGSGLTINKMKEPARRRESLFMRYIINHHPRFK	200
QIAADIINT	ALIFWKRLGARVVGDCREGGPHCMLEGGDFVPVSPGLAMMGVGLRSTYVG	250
CLOADIPER	FEGKDIPFWFNRNDKTSLEGGDELILSKEILAVGISQRTDSASVEKLAKK	250
BACADILIC	GHEIPVWLD RDFKFNIEGGDELVLNEETVAIGVSERTTAQAIERLVRNLF	250
QIAADIINT	AQYLMSKDLLGTRRFVVKDCFDQHQRMHLDCTFSVLHDKLVVLDYYIC	300
CLOADIPER	LLYYPDTSFKTVLAFKIPVSRAFMHLDTVFTQVDYDKFTVHPGIVGPLEV	300
BACADILIC	QRQSRIRRVLA VEIPKSRAFMHLDTVFTMVDRDQFTIHPAIQGPEGDMRI	300
QIAADIINT	SGMGLRYVDEWIDVGADAVKKAKSSAVTCGNYVLAKANVEFQQWLSSENGY	350
CLOADIPER	YALTKDPENDGQLLVTEEVDTLLENILKKYLD RDIKLIKCGGGDEIIAARE	350
BACADILIC	FVLERGKTADEIHTTEEHNLP EVLKRTLGLSDVNLIFCGGGDEIASAREQ	350
QIAADIINT	TIVRIPHEYQLAYGCNNLNLGNNCVLSVHQPTVDFIKADPAYISYCKSNN	400
CLOADIPER	QWNDGSNTLAIAPGEVVVYSRNYVTNEILEKEGIKLHVIPSSSELSRGRGG	400
BACADILIC	WNDGSNTLAIAPGVVVYTYDRNYISNECLREQGIKVIEIPSGELSRGRGGP	400
QIAADIINT	LPNGLDLVYVPFRGITRMYGSLHCASQVVYRTPLAPAAVKACEQEGDGIA	450
CLOADIPER	PRCMSMPLIREDL	413
BACADILIC	RCMSMPLYREDVK	413
QIAADIINT	AIYEKNGEPVDAAGKKFDCVIYIPSSVDDLIDGLKINLRDDAAPSREIIA	500
QIAADIINT	DAYGLYQKLVSEGRVPYITWRMPSPMPVVS LKGAAGAGSLKAVLDKIPQLT	550
QIAADIINT	PFTPKAVEGAPAA YTRYLGLEQADICVDIK	580

FIG. 12

QIAADIINT = *Giardia intestinalis*
 CLOADIPER = *Clostridium perfringens*
 BACADILIC = *Bacillus licheniformis*

The alignment was done on 2 amino acid sequences.

10/10

Alignment

ENTADIFAE	MSHPINVFSEIGKLKTVMLHRPGKELENLMPDYLERLLFDDIPFLEKAQA	50
LACADISAK	MTSPIHVNSEIGKLKTVLLKRPGEVENITPDIMYRLLFDDIPYLPTIQK	50
ENTADIFAE	EHDFAEALLRSKDIEVVYLEDLAAEALINEEVRRQFIDQFLEENIRSES	100
LACADISAK	EHDQFAQTLRDNGVEVLYLENLAAEAIDAGDVKEAFLDKMLNESHKSPQ	100
ENTADIFAE	AKEKVRELMLEIDDNEELIQKAIAGIQKQELPKYEQEFLTDMVEADYPFI	150
LACADISAK	VQAALKDYLISMATLDMVEKIMAGVRTNEIDIKSKALIDVSADDDYPFYM	150
ENTADIFAE	IDMPNLYFTRDNFATMGHGISLNHMYSVTRQRETIFGQYIFDYHPRFAG	200
LACADISAK	DPMPNLYFTRDPAASMGDGLTINKMTFEARQRESMFMEVIMQHHPRFANQ	200
ENTADIFAE	KEVPRVYDRSESTRIEGGDELILSKEVVAIGISORTDAASIEKIARNIFE	250
LACADISAK	GAQVWRDRDHIDRMEGGDELILSDKVLAIGISQRTSAQSIEELAKVLFAN	250
ENTADIFAE	QKLGFKNILAFDIGEHRKFMHLDTVFTMIDYDKFTIHPEIEGGLVVYSIT	300
LACADISAK	HSGFEKILAIKIPHKHAMMHLDTVFTMIDYDKFTIHPIQGAGGMVDTYI	300
ENTADIFAE	EKADGDIQITKEKDTLDNILCKYLHLDNVQLIRCGAGNLTAAAREQWNDG	350
LACADISAK	LEPGNNDKIKITHQTDLEKVLRLDALEVPETLIPCGGGDAVVAPREQWND	350
ENTADIFAE	SNTLAIAPGEVVVYDRNTITNKALEEAGVKLNYPGSELVRGRGGPRCMS	400
LACADISAK	GSNTLAIAPGVVVYDRNYVSNNLRQYGIKVIEVPSELVRGRGGPRCM	400
ENTADIFAE	MPLYREDL	408
LACADISAK	SMPLVRRKT	409

FIG. 13

ENTADIFAE = *Enterococcus faecalis*

LACADISAK = *Lactobacillus sake*